



SEQUENCE LISTING

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Falkner, Falko-Guenter
Borner, Friedrich

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<140> US 09/661,992

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<170> PatentIn Ver. 2.1

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<223> Description of the artificial sequence:primer

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24

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<210> 5
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Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr
1 5 10

<210> 6
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Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr
1 5 10

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Gln Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val
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Gln Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val
1 5 10

<210> 9
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Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val
1 5 10

<210> 13

<211> 13

<212> PRT

<213> Artificial Sequence

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Val Tyr Gly Phe Gly Trp Gly Tyr Glu Val Asn Asp Tyr
1 5 10

<110> 11

<111> 18

<112> PRT

<113> Artificial Sequence

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<400> 11

Glu Glu Glu Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Glu
1 5 10 15

Glu Glu

<110> 13

<111> 18

<112> PRT

<113> Artificial Sequence

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<400> 12

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 13

<211> 18

<212> PRT

<213> Artificial Sequence

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<221> Description of the artificial sequence:CDR3 region

<400> 13

Glu Tyr Gly Glu Gly Tyr Gly Glu Val Asn Glu Tyr Asp Glu Phe Glu
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Trp Glu

<210> 14
<211> 16
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<213> Artificial Sequence

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<400> 14
Val Arg Tyr Arg Asn Arg Tyr Arg Trp Gly Tyr Arg Gly Arg Phe Gly
1 5 10 15

Asp Glu

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<211> 18
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<400> 15
Arg Arg Arg Gly Glu Tyr Gly Val Tyr Trp Asn Gly Asp Phe Tyr Arg
1 5 10 15

Arg Arg

<210> 16
<211> 18
<212> PRT
<213> Artificial Sequence

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<400> 16
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1 5 10 15

Arg Arg

<210> 17
<211> 18
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<213> Artificial Sequence

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<400> 17
Arg Arg Arg Gly Glu Tyr Gly Val Tyr Trp Asn Gly Asp Phe Tyr Arg
1 5 10 15

Arg Arg

<210> 16
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<400> 16
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<310> 19
<311> 18
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<400> 19
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1 5 10 15

Arg Arg

<210> 20
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<213> Artificial Sequence

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<400> 20
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1 5 10 15

Arg Arg

<310> 21
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<320>
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<400> 21
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1 5 10 15

Arg Arg

<210> 22
<211> 18
<212> PRT
<213> Artificial Sequence

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<400> 22
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1 5 10 15

Arg Arg

<210> 23
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<400> 23
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1 5 10 15

Arg Arg

<210> 24
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<220>
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<400> 24
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1 5 10 15

Arg Arg

<210> 25
<211> 18
<212> PRT
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<220>
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1 5 10 15

Arg Arg

<210> 26
<211> 18
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<220>
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<400> 26
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1 5 10 15

Arg Arg

<210> 27
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<213> Artificial Sequence

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<400> 27
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1 5 10 15

Arg Arg

<210> 28
<211> 18
<212> PRT
<213> Artificial Sequence

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<400> 28
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Arg Arg

<210> 29
<211> 18
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<220>
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<400> 29
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Ala Asp Arg

1

5

10

15

Arg Arg

<210> 30
<211> 18
<212> PRT
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<400> 30
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Ala Arg
1 5 10 15

Arg Arg

<210> 31
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 31
Arg Arg Arg Tyr Val Tyr Asn Gly Trp Gly Tyr Phe Glu Gly Ala Arg
1 5 10 15

Arg Arg

<210> 32
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 32
Arg Arg Arg Glu Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 33
<211> 18
<212> PRT
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<400> 33

<400> 37
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Glu Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<410> 38
<411> 18
<412> PRT
<413> Artificial Sequence

<420>
<423> Description of the artificial sequence:CDR3 region

<400> 38
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Glu Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<410> 39
<411> 18
<412> PRT
<413> Artificial Sequence

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<423> Description of the artificial sequence:CDR3 region

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<400> 39
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Glu Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<410> 40
<411> 18
<412> PRT
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<420>
<423> Description of the artificial sequence:CDR3 region

<400> 40
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1 5 10 15

Arg Arg

<410> 41
<411> 18
<412> PRT
<413> Artificial Sequence

<420>
<423> Description of the artificial sequence:CDR3 region

<400> 41
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1 5 10 15

Arg Arg

<210> 42
<211> 18
<212> PRT
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<400> 42
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Glu Arg
1 5 10 15

Arg Arg

<210> 43
<211> 18
<212> PFT
<213> Artificial Sequence

<220>
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<400> 43
Arg Arg Arg Gly Glu Tyr Gly Glu Tyr Trp Asn Gly Asp Phe Tyr Arg
1 5 10 15

Arg Arg

<210> 44
<211> 13
<212> PRT
<213> Artificial Sequence

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<400> 44
Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val
1 5 10

<210> 45
<211> 14
<212> PRT
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<223> Description of the artificial sequence:CDR3 region

<400> 45

Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg
1 5 10

<211> 46

<211> 18

<212> PRT

<213> Artificial Sequence

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<223> Description of the artificial sequence:CDR3 region

<400> 46

Phe Gly Val Gly Tyr Arg Gly Glu Thr Arg Asn Phe Asp Trp
1 5 10

<211> 47

<211> 18

<212> PRT

<213> Artificial Sequence

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<223> Description of the artificial sequence:CDR3 region

<400> 47

Glu Glu Glu Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Glu
1 5 10 15

Glu Glu

<211> 48

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 48

Arg Arg Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<211> 49

<211> 18

<212> PRT

<213> Artificial Sequence

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<223> Description of the artificial sequence:CDR3 region

<400> 49

Arg Arg Arg Phe Gly Val Gly Tyr Gly Glu Thr Asn Phe Asp Trp Arg
1 5 10 15

Arg Arg

<210> 50
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:primer

<400> 50
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<210> 51
<211> 56
<212> DNA
<213> Artificial Sequence

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<223> Description of the artificial sequence:primer

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<210> 52
<211> 56
<212> DNA
<213> Artificial Sequence

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<223> Description of the artificial sequence:primer

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<210> 53
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<212> DNA
<213> Artificial Sequence

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<400> 53
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<210> 54
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:primer

<400> 54
gtcttcgcaa ctgaggccca gccggccatg gccaggtgc agctgcacca rctcgg 56

<210> 55

<211> 56
<212> DNA
<110> Artificial Sequence

<210>
<210> Description of the artificial sequence:primer

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gtctcgcaaa ctgctggccca gccggccatg gccaggttc acctgcagca gctcgg 56

<211> 56
<212> DNA
<110> Artificial Sequence

<210>
<210> Description of the artificial sequence:primer

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gtctcgcaaa ctgctggccca gccggccatg gccaggttc agctggtgga ctctgg 56

<211> 56
<212> DNA
<110> Artificial Sequence

<210>
<210> Description of the artificial sequence:primer

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gtctcgcaaa ctgctggccca gccggccatg gccaggttc agcttcagca gtctgg 56

<211> 56
<212> DNA
<110> Artificial Sequence

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<210> Description of the artificial sequence:primer

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<211> 56
<212> DNA
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<210>
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<211> 60
<212> DNA
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<223> Description of the artificial sequence:primer

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ttggcccc

<210> 61

<211> 60

<212> DNA

<213> Artificial Sequence

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<223> Description of the artificial sequence:primer

<400> 61

accccacagag ggcgcgccac ctgaaccgcc tccacctgag gagacggtga ccgtggtccc 60

<210> 61

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

<400> 61

accccacagag ggcgcgccac ctgaaccgcc tccacctgag gagaactgtga gactggtgcc 60

<410> 63

<210> 60

<212> DNA

<213> Artificial Sequence

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<223> Description of the artificial sequence:primer

<400> 63

accgacagag ggcgcgccac ctgaaccgcc tccacctgag gagacagtga ccagagtccc 60

<210> 64

<211> 60

<212> DNA

<213> Artificial Sequence

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<223> Description of the artificial sequence:primer

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<210> 65

<211> 60

<212> DNA

<213> Artificial Sequence

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<223> Description of the artificial sequence:primer

<11> 65
ggttcagatg ggcgcgcctc tggcggtggc ggatcggaca ttgagctcac acagtctcca 61

<110> 66
<111> 59
<112> DNA
<113> Artificial Sequence

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<223> Description of the artificial sequence:primer

<100> 66
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<110> 67
<111> 59
<112> DNA
<113> Artificial Sequence

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<223> Description of the artificial sequence:primer

<400> 67
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<110> 63
<111> 59
<112> DNA
<113> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

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<110> 69
<111> 59
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<113> Artificial Sequence

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<223> Description of the artificial sequence:primer

<400> 69
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<110> 70
<111> 59
<112> DNA
<113> Artificial Sequence

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<210> 71

<211> 59

<212> DNA

<213> Artificial Sequence

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<223> Description of the artificial sequence:primer

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<210> 72

<211> 54

<212> DNA

<213> Artificial Sequence

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<210> 73

<211> 59

<212> DNA

<213> Artificial Sequence

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<223> Description of the artificial sequence:primer

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<210> 74

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of the artificial sequence:primer

<400> 74

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<210> 75

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of the artificial sequence:primer

<400> 75

gagtcattct ggcgcgcacc gtttgatttc cagcttggtc cc 42

<210> 76
<211> 42
<212> DNA
<213> Artificial Sequence

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<400> 76
gagtcattct ggggcgcgcc gttttatttc cagtctggtc cc 42

<210> 77
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
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<400> 77
gagtcattct ggggcgcgcc gttttatttc caactttgtc cc 42

<210> 78
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
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<400> 78
gagtcattct ggggcgcgcc gtttcagctc cagcttggtc cc 42

<210> 79
<211> 74
<212> DNA
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<223> Description of the artificial sequence:mychis 6

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ggggccagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca 60
ccttcactaa taag 74

<210> 80
<211> 74
<212> DNA
<213> Artificial Sequence

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atttttatt agtgatggtg atggatgatgt gccgccccat tcagatcctc ttctgagatg 60
agttttggtt ctgc 74

<210> 81

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 tcttccaagg ctctctgggtg tatcttcaca aactatggaa tpaactgggt gaagcaggct 120
 ccagaaaagg gttaaaagtg gatggggtgg ataaacacct aaactggaga gccaacatat 180
 gtgatgact tcaagggacg gtttgcttcc tctttggaaa cctctgctag cactgcttat 240
 ttgcagatca acaacctcaa aaatgaggac acggctacat attctgtgc attatatggt 300
 aaatccctta aggggtttgc ttaactggggc caagggactc tggtcactgt ctctgacggt 360
 ggagcgggtt caggtggggc cgcctctggc ggtgggggat cggatattca gatgacacag 420
 tctcccaaat tctgtcttgt atcagcagga gacaggggta ccataacctg caaggccagt 480
 cagactgtga gtaatgatgt agtttggtao caacagaagg cggggccagtc tctaaacta 540
 ctgatgtact atgcattcaa tgcctacaat ggagtccctg atcgcttcac tggcagtgga 600
 tatgggacgg atttcacttt caccatcagc actgttcagg ctgaagacct ggcagtttat 660
 tctctcagc aggtattatg ctctctctcc aggttcggag ggggcaccaa gctggaaatt 720
 aaatcgg 726

<210> 82
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 <212> PRT
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<400> 82
 Glu Val Lys Leu Val Glu Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asn Tyr
 20 25 30
 Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
 50 55 60
 Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
 85 90 95
 Ala Leu Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Arg Ala
 115 120 125
 Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Lys Phe
 130 135 140
 Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
 145 150 155 160
 Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln

165

170

175

Ser Pro Lys Leu Leu Met Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val
180 185 190

Pro Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr
195 200 205

Ile Ser Thr Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln
210 215 220

Asp Tyr Gly Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Arg

<110> 83

<111> 847

<112> DNA

<113> Artificial Sequence

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<123> Description of the artificial sequence:scFv region

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gaagtgagc tgggtggagtc tggggggaggg ctagtgaagc ctggagggtc cctgaaactc 60
tctctgttcag cctctgggatt cactttcagt acctatacca tgtcttgggt tcgcacagact 120
tcggagaaga ggtctggagtg ggtcgcaacc attagtagtg gtggtagtta cactactat 180
cagacagtg tgaggggccc attcaccatc tcacagagaca atgccaagaa cactctgtac 240
ctgcaatga gcagtctgaa gtctgaggac acagccatgt attactgtac aagagatggg 300
ggacgggt acggtagtag ctctgactac tggggccaag gcaccactct cacagtctcc 360
tcaggtggag ggggttcagg tggggggccc tctggcggtg ggggatcgca aattgtgtc 420
acccagtctc cactctccct gctgtcagt ctggagatc aagcctccat ctcttgaga 480
tcagtcaga gcattgtaca tagtaatgga aacacctatt tagaatggta cctgcagaaa 540
tcagccagt ctccaaagct cctgatctac aaagtctcca accgattttc tggggtccca 600
gcacattca gtggcagtggt atcagggaca gatttcacac tcaagatcag cagagtggag 660
gtgaggatc tgggagttta ctactgttt caaggttcac atgttcogtg gacgttcggt 720
gagtcacca agctggaaat caaacgg 747

<110> 84

<111> 249

<112> PRT

<113> Artificial Sequence

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<123> Description of the artificial sequence:scFv region

<400> 84

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Thr Arg Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125
 Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro
 130 135 140
 Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
 145 150 155 160
 Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp
 165 170 175
 Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
 180 185 190
 Ser Asn Arg Phe Ser Gly Val Pro Asp Lys Phe Ser Gly Ser Gly Ser
 195 200 205
 Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
 210 215 220
 Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly
 225 230 235 240
 Gly Gly Thr Lys Leu Glu Ile Lys Arg
 245

<210> 85

<211> 247

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: scFv region.

<240> 85

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 ctggagaaga ggtctggagt gctcgcaacc attagtagtg ttggaggttc caactactat 180
 ctgagacagt tgaagggccg attcaccatc tccagagaca atgccaagaa caccctgtac 240
 ctgcaaatga gaagtctgag gtctgaggac acagccatgt attactgtac aagagagggg 300
 ggtggtttca cgttcaactg gtacttcgat gtctggggcg cagggactct ggtcactgtc 360
 tctgcaggtg gaggggttc aggtggggcg gctctggcg ttgggggata tgaaaaatgtg 420
 ctcccccagt ctccagcttc ttgtgctgtg tctctagggc agagggcac cctatcctgc 480
 agagccagtg aaagtgtga tagttatggc tataatttta tgcactggta ccagcaata 540
 ctaggacagc cccccaaact cctcatctat cgtgcaccca acctagagtc ttggatccct 600
 gtcaggttca gtggagtggt gctcaggaca caattcaccc tcaccattaa tctgtggag 660
 gctgatgatg ttgcaacctc ttactgtcag caaagtaatg aggatccgct cactgttggg 720
 actgggacca gactggaaat aaaacgg 747

<210> 86

<211> 249

<212> FRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 66

Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Thr Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val Trp
100 105 110

Gly Ala Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly
115 120 125

Gly Arg Ala Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser
130 135 140

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
145 150 155 160

Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Tyr Asn Phe Met His Trp
165 170 175

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala
180 185 190

Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
195 200 205

Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
210 215 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly
225 230 235 240

Thr Gly Thr Arg Leu Glu Ile Lys Arg
245

<210> 87

<211> 747

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 57

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caggagaaga ggtctggagt ggtcgcaacc attagtatgt gtggtagtto cactactat 147  
ccagacagt tgaaggggccg attcaccatc tccagagaca atgccaagaa caccctgtac 147  
ctgcaaatga gcagtctgaa gtctgaggac acagccatgt atcactgtac aagagagggg 173  
gtgtgttatt acgtcaactg gtaattogat gtctggggcg caggcaccac tctcagatc 173  
tctcaggtg gaggggggtc aggtggggcg gctctggcg gtgggggac ggcattgag 427  
ctcaccagc ctcagcttc tttgctgtg tctctaggcg agaggggcac catatctgt 447  
agagccagt aaagtgttga tagttatggo aagagtttta tgcactggta ccagcagaaa 547  
ccagggcagc cacccaaaact cctcatttat cgtgcattca acctagaatc tgggatccct 600  
cccaggttca gtggcagtg gtctaggaca gacttcacc tcaccattaa tctctggag 660  
gtgtgtgtg ttgcnacctt ttaactgtac caaagtaatg aggatccct cactctgggt 720  
gttgggacca gactgaaat aaaaagg 747
```

<210> 88

<211> 249

<212> FRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 88

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Glu Val Gln Leu Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly  
1 5 10 15  
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr  
20 25 30  
Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val  
35 40 45  
Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr His Cys  
85 90 95  
Thr Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val Trp  
100 105 110  
Gly Ala Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Ser Gly  
115 120 125  
Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser  
130 135 140  
Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys  
145 150 155 160  
Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Lys Ser Phe Met His Trp  
165 170 175  
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala  
180 185 190  
Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
```

195

200

205

Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
210 215 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Arg Leu Glu Ile Lys Arg
245

<210> 9

<211> 1199

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 9

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atgaaataacc tattgcctac ggcagccgct ggatgttat tactcgggc ccagccggcc 60
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aaccctcct ggcagcctc tgatctcact tccagtagct ataccatgtc ttgggttcgc 180
cagactccg agaagaggtt gtagtgggtc gaaacatta gtagtggngg tagttccacc 240
tactatccag aagatgtgaa ggcgcgattc accatctcc gagacattgc caagaacacc 300
ctgttcctgc aatgagcag ttgaggttc gaggacacag ccatgtatta ctgtacaaga 360
gagggggtg gttccacgt ccaatgggtc ttgaggtct ggaggcgaag aacctcagtc 420
aaggttcctt caggtggag cgttcagtc gggcgcgct ctggggttg cggatcggac 480
atgtgttga cagatctcc agttctttg gctgtcttc tagggcag aggccaccata 540
tctgtcagag cagtgaaag ttctgataat tatgtctata attttatgca ctggtatcag 600
cagatctcag gacagccacc caaacctccc atctatcgtg caccacacc agagtctgg 660
atctctgcca gttcagttg cagtggtctt aggcagact tcaccctcac cattaactt 720
ggcgaggctg abgatgttc aacctattac ttgcagcaaa gtaatgagja tccgctcag 780
tctggtactg gaaacagact gaaataaaaa cggcgcgcc cagcccggg accagaaatg 840
ctggttcgg gaaacggggc tctcagggc gatattact tacccgggc tctcgcctt 900
ttaaaggtg atcagactgc cgtctcgcct gathctctta tgcataaaac tgcataaaat 960
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atcactatg cgtgcaata aaaaacggg taacggact tctcaccja ctcggttga 1140
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cagcaaaaag atcaccacac gattctggaa atggcaaaa cgcaggtct ggcgaccgt 1260
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ctcgtatgag cgtacaaag ggcgttgaa ttcttcaaaa aggaggtta cagcttggt 1920
atagtcacg ctgatacgc ccacgcgcg tagattgtt cgcgggata caaagctcc 1980
ggcttcacc aggcgtataa taccaaaat ggcgcagtga tgggtatgac ttacgggaac 2040
tccgaagagg attcacaaga acataccggt agtcagttgc gtattgcgc gtatggcgc 2100
catccgcga atgttcttg actgacggc cagaccgat tctctacac catgaaagc 2160
gctctgctgg atatcgaca ccatcaccat caccattaa 2199

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<210> 90

<211> 732

<212> BHT

<213> Artificial Sequence

<213>

<213> Description of the artificial sequence:scFv region

<411> 30

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Phe Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
65 70 75 80

Tyr Tyr Phe Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
85 90 95

Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp
100 105 110

Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Gly Phe Thr Val Asn
115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser
130 135 140

Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp
145 150 155 160

Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
165 170 175

Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly
180 185 190

Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
195 200 205

Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg
210 215 220

Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro
225 230 235 240

Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
245 250 255

Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala
260 265 270

Ala Ala Ala Arg Ala Pro Glu Met Pro Val Leu Gln Asn Arg Ala Ala
275 280 285

Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp
290 295 300

Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn
 305 310 315 320
 Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala
 325 330 335
 Ala Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp
 340 345 350
 Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys
 355 360 365
 Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala
 370 375 380
 Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile
 385 390 395 400
 His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly
 405 410 415
 Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro
 420 425 430
 Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser
 435 440 445
 Ala Thr Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys
 450 455 460
 Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu
 465 470 475 480
 Gly Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp
 485 490 495
 Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu
 500 505 510
 Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln
 515 520 525
 Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp
 530 535 540
 Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val
 545 550 555 560
 Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala
 565 570 575
 Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly
 580 585 590
 Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala
 595 600 605
 Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala
 610 615 620
 Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val
 625 630 635 640

Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp
645 651 655

Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala
660 665 670

Val Met Val Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Glu His
675 680 685

Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn
690 695 700

Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala
705 710 715 720

Ala Leu Gly Asp Ile Ala His His His His His His
725 730

<210> 91

<211> 973

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 91

atgaatacc tattgactac ggcagccgct ggattgttat tactcgggga ccagccggcc 60
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aaactctctt ggcagcctc tggattcaat ttcagtagct ataccatgtc ttgggttcgc 180
caactctcgg agaagaggct ggagtgggct gcaaccatta gtatggngg tagttccacc 240
tactctccag acagtgtgaa ggcccgatcc accatctcca gagacaatgc caagaacacc 300
ctgtacctgc aaatgagcag cctgaggtct gaggacacag ccattgtatta ctgtacaaga 360
gagcgggggtg gtttccactt caactggtag ttgatgtct ggggggcagg aacctcagtc 420
aaactctctt caggtggagg cggttcaggt gggcggcct ctggcgggtg cggatcggac 480
attgtgctga cacagctcc agcttctttt gctgtgtctc tagggcagag ggccaccata 540
tcctccagag ccagtgaag tttgatagt tatggctata atttcatgca ctggtatcag 600
cagataccag gacagccacc caaactctct atctatctgt catccaaact agagtctggg 660
atcctctcca ggttcaagt ggtgggtct aggaacagct tcacctccac cattaatctt 720
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caccaccatc accattaa 978

<210> 92

<211> 325

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 92

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly

35

40

45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
85 90 95

Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp
100 105 110

Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Gly Phe Thr Val Asn
115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser
130 135 140

Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp
145 150 155 160

Ile Val Leu Thr Gln Xaa Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
165 170 175

Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly
180 185 190

Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
195 200 205

Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg
210 215 220

Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro
225 230 235 240

Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
245 250 255

Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala
260 265 270

Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln
275 280 285

Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu
290 295 300

Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His
305 310 315 320

His His His His His
325

<10> 93

<11> 2190

<12> DNA

<13> Artificial Sequence

<20>

<123> Description of the artificial sequence:scFv region

<400> 94

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aagatttcctt gcaaaagcttc tggctacgca ttcagtagct ctgggatgaa ctgggtgaa 181
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aactacaatg ggaagttcaa gggcaaggcc acactgaatg cagacaaatc ctccagcaca 301
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gacaccccaa gattcttga aatggcaaaa gcgpcaggtc tggcgacggg taaggtttct 1260
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gctgtccag cccatggcag ccagattgtt aggcgggata ccaaaagctcc gggcctcacc 1980
caggcgctaa ataccaaaag tggcgagtg atggtgatga gttacgggaa ctccgaagag 2040
gattcacag aacataccgg cagtcagttg cgtattggcg cgtatggccc gcattccgct 2100
aattgtgttg gaactgacga ccagacgat ctctctatca ccattgaaagc cgtctggtgg 2160
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```

<11> 94

<11> 729

<12> FRT

<13> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 94

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Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
1           5           10          15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
20          25          30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
35          40          45

Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
50          55          60

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Gln	Gly	Leu	Ala	Trp	Ile	Gly	Arg	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr		
65					70					75					80		
Asn	Tyr	Asn	Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys		
				85					90					95			
Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Val	Asp		
			100					105					110				
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Asp	Gly	Asn	Val	Tyr	Tyr	Tyr	Ala	Met		
	115						120					125					
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly		
	130					135						140					
Gly	Ser	Gly	Gly	Arg	Ala	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Ile	Val	Leu		
145					150					155					160		
Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr		
				165					170					175			
Ile	Ser	Cys	Arg	Ala	Ser	Lys	Ser	Val	Ser	Thr	Ser	Gly	Tyr	Ser	Tyr		
		180						185					190				
Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile		
	195						200					205					
Tyr	Leu	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly		
	210					215					220						
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His	Pro	Val	Glu	Glu		
225					230					235				240			
Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	His	Ser	Arg	Glu	Leu	Pro	Arg		
				245					250					255			
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Ala	Ala	Ala		
		260						265					270				
Arg	Ala	Pro	Glu	Met	Pro	Val	Leu	Glu	Asn	Arg	Ala	Ala	Gln	Gly	Asp		
	275						280					285					
Ile	Thr	Ala	Pro	Gly	Gly	Ala	Arg	Arg	Leu	Thr	Gly	Asp	Gln	Thr	Ala		
	290					295					300						
Ala	Leu	Arg	Asp	Ser	Leu	Ser	Asp	Lys	Pro	Ala	Lys	Asn	Ile	Ile	Leu		
305					310					315					320		
Leu	Ile	Gly	Asp	Gly	Met	Gly	Asp	Ser	Glu	Ile	Thr	Ala	Ala	Arg	Asn		
			325						330					335			
Tyr	Ala	Glu	Gly	Ala	Gly	Gly	Phe	Phe	Lys	Gly	Ile	Asp	Ala	Leu	Pro		
		340					345						350				
Leu	Thr	Gly	Gln	Tyr	Thr	His	Tyr	Ala	Leu	Asn	Lys	Lys	Thr	Gly	Lys		
	355						360					365					
Pro	Asp	Tyr	Val	Thr	Asp	Ser	Ala	Ala	Ser	Ala	Thr	Ala	Trp	Ser	Thr		
	370					375					380						
Gly	Val	Lys	Thr	Tyr	Asn	Gly	Ala	Leu	Gly	Val	Asp	Ile	His	Glu	Lys		
385					390					395					400		

Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr
 405 410 415
 Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu
 420 425 430
 Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser
 435 440 445
 Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile
 450 455 460
 Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly
 465 470 475 480
 Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys
 485 490 495
 Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp
 500 505 510
 Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu
 515 520 525
 Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro
 530 535 540
 Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr
 545 550 555 560
 Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr
 565 570 575
 Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu
 580 585 590
 Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro
 595 600 605
 Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg
 610 615 620
 Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr
 625 630 635 640
 Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala
 645 650 655
 Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val
 660 665 670
 Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser
 675 680 685
 Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly
 690 695 700
 Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly
 705 710 715 720
 Asp Ile Ala His His His His His
 725

<210> 95
 <211> 969
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Description of the artificial sequence:scFv region

<400> 95
 atgaaatacc tattgootac ggcagccgct ggattgttat tactcggggc ccagccgggc 61
 atggcggagg tttagcttca gcagtctgga cctgagctgg tgaagccggg ggootcagtg 120
 aagatttccct gcaaaagcttc tggctacgca tttagtagct cttggatgaa ctgggtgaag 180
 cagaggootg gacagggtct tgagtggatt ggaaggattt atctggaaa tggagatact 240
 aactacaatg ggaagttcaa gggcaaggcc acactgactg cagacaaatc ctccagcaca 300
 gctacatgc agtcagcag cctgacctct gtggactctg cgtctatatt ctgtgcagat 360
 ggtaacgtat attactatgc tatggactac tggggtaag gaaactcagt cactgtctcc 420
 tcaggtggag gcgttcagg tgggcggccc tctggcgtg gcggatcgca aattgttccc 480
 accagctctc ctgttccctt agctgtatct ctggggcaga gggccacct ctcatgcagg 540
 gcaagcaaaa ctgtcagtac atctggctat agttatatgc actggtacca acagaaacca 600
 ggaacagcac ccaaaactct catctatctt gcacccaacc tagaatctgg ggtccctgcc 660
 aggttcagtg gcagtggttc tgggacagac ttacacctca acatccatcc tgtggaggag 720
 caggatgctg caacctatta ctgtcagcac agtagggagc ttctcggac gttcgttga 780
 ggaacaaagc tggaaatcaa acggggggcc gcaccgaagc cttccactcc gccgggtct 840
 tccctatga accagctgga agacaaagta gaggagctcc tttagcaaga ctaccatcta 900
 caaacagagg tagctcgtct gaaaaagctt gthggtgaac gtggtggtca ccataccat 960
 caccattaa 969

<210> 96
 <211> 322
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> Description of the artificial sequence:scFv region

<400> 96
 Met Lys Tyr Leu Ieu Pro Thr Ala Ala Gly Ieu Ieu Leu Leu Ala
 1 5 10 15
 Ala Gln Pro Ala Met Ala Glu Val Gln Ieu Gln Ser Gly Pro Glu
 20 25 30
 Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Iys Ala Ser Gly
 35 40 45
 Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
 50 55 60
 Gln Gly Ieu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
 65 70 75 80
 Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
 85 90 95
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
 100 105 110
 Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met
 115 120 125
 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly

130	135	140
Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu		
145	150	155
Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr		
	165	170
Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr		
	160	180
Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile		
	195	200
Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly		
	210	220
Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu		
	225	235
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg		
	245	250
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Pro		
	260	270
Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln Leu Glu Asp		
	275	285
Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val		
	290	300
Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His His His His		
	305	315
His His		320

<210> 97
 <211> 270
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of the artificial sequence:scFv region

<400> 97
 caggaaacag ctatgaccat gattaagcga agcttccatg aaaattctat ttcaaggaga 60
 cagtcataat gaaataaccta ttgcctacgg cagccgctgg attgttatta ctgcgggcc 120
 agccggccat ggcccaggtg cagctgcagg cgcgcctgca ggtcgacctc gagatcaaac 180
 ggccggccgc agaacaaaaa ctatctcag aagaggatct gaatggggcg gcacatcac 240
 atcaccatca ctaataagaa ttaactggcc 270

<210> 98
 <211> 61
 <212> FRT
 <213> Artificial Sequence

<220>
 <223> Description of the artificial sequence:scFv region

<400> 98

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Ala Arg Leu Gln Val
20 25 30

Asp Leu Ala Ile Lys Arg Ala Ala Ala Gln Gln Lys Leu Ile Ser Gln
35 40 45

Glu Asp Leu Asn Gly Ala Ala His His His His His His
50 55 60

<210> 99

<211> 888

<212> DNA

<213> Artificial Sequence

seq

<213> Description of the artificial sequence:scFv region

<400> 99

cgagataacc tattgacctac ggcagcgcgt ggattgttat tactcggggc ccagccggcc 81
tggccgaggg tgaagctggg ggagctctgg ggaggttag tgaagctgg agggctcccg 120
aaactctctt gtcagacctc tggattcact tttagtagct ataccatgtc ttgggttcgc 160
cagactccgg agaagagggt ggagtggttc gcaaccatta gtatggngg tagttccacc 240
tactatccag acagtgtgaa gggccgatto accatctcca gagacaatgc caagaacacc 300
ctgtaccctg aaatgagcag tctgaggtct gaggacacag ccattgtatta ctgtacaaga 360
gagggggggt gttccacctt caactgggtt ttcgatgtct gggggcagg aacctcagtc 420
aacgtctctt caggtggagg cggttccaggt gggcgggct ctggcggttg cggatcggac 480
atttgtctga cacagtcttc agctctcttg gctgtctctc tagggagag ggcaccata 540
tctgtcagag ccagtgaag tttgatagt tatggtata attttatgca ctggtatcag 600
cagataccag gacagccacc caaatctctc atcatcgtg catccaaact agagtctggg 660
atccctgcca ggttcagtg cagtgggtct aggaagact ccacctccac cattaactct 720
tggcaggctg atgagtctg aacctattac tgtacgaaa gtaatgagga tccgctcag 780
tccgtactg ggcacagact ggaataaaaa cggcgggcgc cagaacaaaa actcatctca 840
gaagaggatc tgaatggggc ggcacatcac catcacatc actaataa 888

<210> 100

<211> 294

<212> PRT

<213> Artificial Sequence

<210>

<213> Description of the artificial sequence:scFv region

<400> 100

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
 85 90 95
 Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp
 100 105 110
 Thr Ala Met Tyr Tyr Cys Thr Arg Gln Gly Gly Gly Phe Thr Val Asn
 115 120 125
 Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser
 130 135 140
 Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp
 145 150 155 160
 Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
 165 170 175
 Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly
 180 185 190
 Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
 195 200 205
 Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg
 210 215 220
 Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro
 225 230 235 240
 Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
 245 250 255
 Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala
 260 265 270
 Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 275 280 285
 His His His His His
 290

<210> 101

<211> 876

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 101

atgaaatacc tattgcttac ggcagccgct ggattgttat tactggcggc ccagccggcc 40
 atgpcgagg ttccagcttca gcagtcgga cctgagctgg tgaagccggg ggccctagtg 120
 aagatttcct gcaaaagctt tggtacgca ttcagtagct ctgggatgaa ctgggtgaag 160
 cagaggcctg gacagggtct tgagtggtatt ggaaggattt atcctggaaa tggagatact 240
 aactacaatg ggaagttcaa gggcaaggcc acactgaact cagacaaaac ctccagpaca 300
 gctacatgc agctcagcag cctgacctct gtggactctg cgtctatatt ctgtgcagat 360
 ggtaacgtat attactatgc tatggactac tggggtcaag gaacctcagt caccgtctcc 420
 tcaggtggag ggggttcagg tggggcgccc tctggcggtg ggggatgca aattgtctc 480
 acccagtttc ctgcttcctt agctgtatct ctgggcaga gggccaccat ctcatgcagg 540
 gccagcaaaa gtgtcagtac atctggctat agttatatgc actggtacca acagaaacca 600

ggacagccac ccaaaactcct catctatctt gcacccaacc tagaatctgg ggtccctgac 101
 aggttcagtg gaagtgggtc tgggacagac ttccacctca acatccatcc tctggaggag 110
 gaggatgctg caacctatta ctgtcagcac agtagggagc ttccctggac gttcggggga 120
 ggcaccaagc tggaaatcaa acgggggggc gcagaacaaa aactcatctc agaagaggt 130
 ctgaatggg ggcacatca ccatcaccat cactaa 140

<210> 102

<211> 221

<212> ERT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 102

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
 20 25 30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
 35 40 45

Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
 50 55 60

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
 65 70 75 80

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
 85 90 95

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
 100 105 110

Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met
 115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu
 145 150 155 160

Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
 165 170 175

Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 180 185 190

Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 195 200 205

Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
 210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
 225 230 235 240

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg
 245 250 255

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu
261 265 271

Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His His His
276 280 285

His His His
290

<210> 103
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<400> 103
gggggcagaa caaaaactca tctcagaaga ggatctgaat ggggcggcac atcaccatca 60
caactactaa taag 74

<210> 104
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<400> 104
ttattagtga tgggtgatggt gatgtgccgc cccattcaga tctctctctg agatgagttt 60
tggctctgc 69

<210> 105
<211> 15
<212> FRT
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:CDR3 region

<400> 105
Cys Xaa Xaa Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Xaa Xaa Cys
1 5 10 15

<210> 106
<211> 16
<212> FRT
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:CDR3 region

<400> 106
Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asx
1 5 10 15